

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2003, 10:59:02 : Search time 11.364 Seconds
(without alignments)
1025.596 Million cell updates/sec

Title: US-09-508-849a-17

Perfect score: 1523

Sequence: 1 MQQPNVPPYQIYWDSSAS.....SELVLNFEESQTFGLYKL 281

Scoring table:

BLAST62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1523	100.0	281	1	TNFB_HUMAN
2	1473.5	96.7	280	1	TNFB6_MACRO
3	1469.5	96.5	280	1	TNFB6_MACRO
4	1295.5	85.1	282	1	TNFB6_PIG
5	1156	75.9	279	1	TNFB6_MOUSE
6	1136.5	74.6	278	1	TNFB6_MOUSE
7	250	16.4	239	1	TNFB6_MOUSE
8	224.5	14.7	240	1	TNFB6_MOUSE
9	205	13.5	202	1	TNFB6_MOUSE
10	204	13.4	202	1	TNFB6_MOUSE
11	202.5	13.3	205	1	TNFB6_MOUSE
12	200.5	13.2	201	1	TNFB6_MOUSE
13	200.5	13.2	291	1	TNFB6_MOUSE
14	200	13.1	197	1	TNFB6_MOUSE
15	193.5	12.7	174	1	TNFB6_MOUSE
16	191	12.5	205	1	TNFB6_MOUSE
17	189	12.4	317	1	TNFB6_MOUSE
18	186.5	12.2	234	1	TNFB6_MOUSE
19	186	12.2	233	1	TNFB6_MOUSE
20	186	12.2	281	1	TNFB6_MOUSE
21	185.5	12.2	232	1	TNFB6_MOUSE
22	185	12.1	233	1	TNFB6_MOUSE
23	184	12.1	204	1	TNFB6_MOUSE
24	183.5	12.0	204	1	TNFB6_MOUSE
25	183	12.0	233	1	TNFB6_MOUSE
26	183	12.0	272	1	TNFB6_MOUSE
27	181	11.9	233	1	TNFB6_MOUSE
28	180	11.8	233	1	TNFB6_MOUSE
29	179	11.7	233	1	TNFB6_MOUSE
30	177	11.6	141	1	TNFB6_MOUSE
31	176	11.6	233	1	TNFB6_MOUSE
32	176	11.6	233	1	TNFB6_MOUSE
33	175.5	11.5	229	1	TNFB6_MOUSE

34	174	11.4	233	1	TNFB6_MOUSE	077764 macropus eu
35	174	11.4	233	1	TNFB6_MOUSE	P48094 macaca mla
36	173.5	11.4	316	1	TNFB6_MOUSE	O35235 m tumor nec
37	172.5	11.3	318	1	TNFB6_MOUSE	O35235 r tumor nec
38	171.5	11.3	415	1	TNFB6_MOUSE	O35235 r tumor nec
39	171	11.2	233	1	TNFB6_MOUSE	P08001 sus scrofa
40	170	11.2	233	1	TNFB6_MOUSE	P79337 macaca fasc
41	169.5	11.1	485	1	TNFB6_MOUSE	O77510 papio hamad
42	168.5	11.1	235	1	TNFB6_MOUSE	P21997 volvox cart
43	166.5	10.9	234	1	TNFB6_MOUSE	P44924 oryctolagus
44	165.5	10.9	389	1	TNFB6_MOUSE	P13296 capra hircu
45	165	10.8	233	1	TNFB6_MOUSE	O03173 mus musculu
						P19101 felis silve

ALIGNMENTS

RESULT 1	ID	TNFB_HUMAN	STANDARD	PRT:	281 AA.
AC	P48023	Q9BZP9			
DT	01-FEB-1996	(Rel. 33, Created)			
DT	01-FEB-1996	(Rel. 33, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)				
DE	(Apoptosis antigen ligand) (APL) (CD178 antigen).				
GN	TNFB6 OR FASL OR APTL1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxId=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=95105731; PubMed=7528780;				
RA	"Fas ligand mediates activation-induced cell death in human T				
RT	lymphocytes";				
RL	J Exp. Med. 181:71-77(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=95127560; PubMed=7826947;				
RA	"Takashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;				
RT	"Human Fas ligand: gene structure, chromosomal location and species				
RL	specificity";				
RN	Int. Immunol. 6:1567-1574(1994).				
RP	[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RA	Schaeuble C.E., Poehmann R., Philippson P., Eidel H.;				
RT	Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=95071350; PubMed=7980502;				
RA	Mita E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara A.;				
RT	Fusamato H., Kaneda T.;				
RL	"Role of Fas ligand in apoptosis induced by hepatitis C virus				
RP	infection";				
RN	Biochem. Biophys. Res. Commun. 204:468-474(1994).				
RP	[5]				
RP	SEQUENCE FROM N.A. (ISOFORM 2).				
RA	Tissue-Lymphocyte;				
RT	Zeytun A., Nagarkatti M., Nagarkatti P.S.;				
RL	"Isolation and characterization of a new naturally occurring variant of				
RP	human Fas ligand that is expressed only in membrane bound form";				
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.				
RN	[6]				
RP	SEQUENCE FROM N.A.				
RA	Wilkinson J.;				
RT	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.				
RN	[7]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RA	Tissue-Blood;				
RT	Strausberg R.;				
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.				

RN [8] SEQUENCE OF 1-10 FROM N.A.
 RP TISSUE-Blood;
 RA Matsumura M., Nakanishi Y., Ohba Y.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
 RX PubMed=9228058;
 RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,
 RA Terstik A., Peitsch M.C., Tschopp J.;
 RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction."; *J. Biol. Chem.* 272:18827-18833(1997).
 RN [10]
 RP PROCESSING.
 RX PubMed=9427603;
 RA Tanaka M., Itai T., Adachi M., Nagata S.;
 RT "Downregulation of Fas ligand by shedding."; *Nat. Med.* 4:31-36(1998).
 RL
 CC -1- FUNCTION: Cytokine that binds to TNFRSF6/Fas, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/Fas-mediated apoptosis may have a role in the induction of peripheral tolerance. In the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3 modulates its effects.
 CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL SURFACE.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, 1 (shown here) and 2; are produced by alternative splicing.
 CC -1- PTM: N-glycosylated.
 CC -1- PTM: The soluble form derives from the membrane form by proteolytic processing.
 CC -1- DISEASE: Defects in TNFRSF6 are a cause of autoimmune lymphoproliferative syndrome (ALPS), also known as Canale-Smith syndrome (CSS), a childhood syndrome involving hemolytic anemia and thrombocytopenia with massive lymphadenopathy and splenomegaly.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -1- DATABASE: NAME=PRO; NOTE=PROW 2:59-69(2001);
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/3338769674_g.htm".
 CC
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 CC -----
 CC EMBL: X89102; CAA61474.1; -
 CC EMBL: U08137; AAC50071.1; -
 CC EMBL: U11821; AAC50124.1; -
 CC EMBL: D38122; BAA07320.1; -
 CC EMBL: AF288573; AAG60017.1; -
 CC EMBL: Z96050; CAB09424.1; -
 CC EMBL: BC017502; AAH17502.1; -
 CC EMBL: AB013303; BAA32542.1; -
 CC HSSP: P01375; ITNF.
 CC DR GeneW: HGNC:11936; TNFRSF6.
 CC MIM: 134638; -
 CC MIM: 601859; -
 CC InterPro: IPR003636; TNF_abc.
 CC InterPro: IPR000478; TNF_family.
 CC Pfam: PF00229; TNF; 1.
 CC ProDom: PD002012; TNF_abc; 1.
 CC SMART: SM00207; TNF; 1.
 CC PROSITE: PS00251; TNF_1; 1.
 CC PROSITE: PS0049; TNF_2; 1.
 CC Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
 CC Alternative splicing; Antigen.
 FT CHAIN 1 281 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

FT CHAIN 130 281 MEMBER 6, MEMBRANE FORM.
 FT DOMAIN 1 80 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT TRANSMEM 81 102 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 103 281 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
 FT DOMAIN 4 70 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 45 65 PRO-RICH.
 FT SITE 129 130 POLY-PRO.
 FT DISULFID 202 233 CLEAVAGE.
 FT CARBOHYD 184 184 POTENTIAL.
 FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 117 127 STOMATASL -> ATPVPLPKRS (IN ISOFORM 2).
 FT VARSPPLIC 128 281 MISSING (IN ISOFORM 2).
 FT MUTAGEN 206 206 P->D,F,R: LOWERS BINDING TO TNFRSF6 AND REDUCES CYTOTOXICITY MORE THAN A HUNDREDFOLD.
 FT MUTAGEN 218 218 Y->F,R: LOWERS BINDING TO TNFRSF6 AND ABOLISHES CYTOTOXICITY.
 FT MUTAGEN 275 275 F->L: ABOLISHES BINDING TO TNFRSF6 AND CYTOTOXICITY.
 FT SEQUENCE 281 AA: 31485 MW: 48A6EB358246E9DB CRC64;
 SQ
 Query Match 100.0%; Score 1523; DB 1; Length 281;
 Best local Similarity 100.0%; Pred. NO. 3.1e-97;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 QY 1 MOQFNYPPYPOIYWDSSASSFPAPPGYVLPCTSYRRRPGORRRPPPPPLPPPP 60
 DB 1 MOQFNYPPYPOIYWDSSASSFPAPPGYVLPCTSYRRRPGORRRPPPPPLPPPP 60
 QY 61 PPLPPLPPLPKRGHSTGCLLVFVFWLVALVGLGMFLHQLKELAELESTSQ 120
 DB 61 PPLPPLPPLPKRGHSTGCLLVFVFWLVALVGLGMFLHQLKELAELESTSQ 120
 QY 61 PPLPPLPPLPKRGHSTGCLLVFVFWLVALVGLGMFLHQLKELAELESTSQ 120
 DB 121 MHTASLEKQIGHSPPEPKELRYVAHLTGKSNRSMPLMEDYGIYLLSGVKKKG 180
 QY 121 MHTASLEKQIGHSPPEPKELRYVAHLTGKSNRSMPLMEDYGIYLLSGVKKKG 180
 DB 121 MHTASLEKQIGHSPPEPKELRYVAHLTGKSNRSMPLMEDYGIYLLSGVKKKG 180
 QY 181 LVINENGGLFYVSKYFRQSCNNPLSKRYVRNRSKYRQDLYVMGKKMSCTTGQMA 240
 DB 181 LVINENGGLFYVSKYFRQSCNNPLSKRYVRNRSKYRQDLYVMGKKMSCTTGQMA 240
 QY 241 RSSYLGAVFNLTSAHLYVNSLSLVNFEESOTFFGLTKL 281
 DB 241 RSSYLGAVFNLTSAHLYVNSLSLVNFEESOTFFGLTKL 281
 RESULT 2
 TNF6.CERTO
 ID TNF6.CERTO STANDARD: PRT: 280 AA.
 AC Q9BDN1;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Tumor necrosis factor ligand superfamily member 6 (Fas antigen ligand) (CD95L protein).
 GN TNFRSF6 OR FASL OR CD95L.
 OS Cercopithecus torquatus alyx (Red-crowned mangabey) (sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Boslik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate

RT Fas/Fas-ligand and co-stimulatory molecules.*;
 RL Immunogenetics 53:315-328(2001).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF8/DCR3
 CC modulates its effects (By similarity).
 CC -1- SUBUNIT: Homotrimer (Probable).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 CC similarity).
 CC -1- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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 CC or send an email to license@isb-sib.ch).

 CC EMBL: AF344847; AAK37606.1; -
 CC HSSP: P01375; 4TSV.
 CC InterPro: IPR003636; TNF_abc.
 CC InterPro: IPR000478; TNF_family.
 CC Pfam: PF00229; TNF_1.
 CC PRINTS: PR01234; TNECROSISFCT.
 CC PRODOM: PD002012; TNF_abc; 1.
 CC SMART: SM00207; TNF_1.
 CC PROSITE: PS00251; TNF_1; 1.
 CC PROSITE: PS50049; TNF_2; 1.
 CC Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
 CC CHAIN 1 280
 CC FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 CC FT MEMBER 6, MEMBRANE FORM.
 CC FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 CC FT MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
 CC FT CYTOPLASMIC (POTENTIAL).
 CC FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC FT (POTENTIAL).
 CC FT EXTRACELLULAR (POTENTIAL).
 CC FT PRO-RICH.
 CC FT POLY-PRO.
 CC FT CLEAVAGE (BY SIMILARITY).
 CC FT POTENTIAL.
 CC FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 183 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;

 CC Query Match 96.7%; Score 1473.5; DB 1; Length 280;
 CC Best Local Similarity 97.5%; Pred. No. 7.2e-94;
 CC Matches 274; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

 QY 1 MOOPFNVPYQIYWVSSASSPAPPGTVPCTSVRRPGRORPPPPPPPPPPPPPPPPPP 60
 Db 1 MOOPFNVPYQIYWVSSASSPAPPGTVPCTSVRRPGRORPPPPPPPPPPPPPPPPPP 59
 QY 61 PPLPPLPPLPPLKRGHSTGLCLVMEFVVALVGLGMFOFLHOKELAELESTSQ 120
 Db 60 PPLPPLPPLPPLKRGHSTGLCLVMEFVVALVGLGMFOFLHOKELAELESTSQ 119
 QY 121 MHTASSLEKQIGHPSPPEKELRYAHLTGKSNRSMPLMEDETVIVLSGVKRYKGG 180
 Db 120 KHTASSLEKQIGHPSPPEKELRYAHLTGKSNRSMPLMEDETVIVLSGVKRYKGG 179
 QY 181 LVINETGLYEVYSKVYRGGSCNNLPLSHKYVMNSKYPDDIVYMEKMMSYCTTGOMMA 240
 Db 180 LVINETGLYEVYSKVYRGGSCNNLPLSHKYVMNSKYPDDIVYMEKMMSYCTTGOMMA 239
 QY 241 RSSYLGAVENTLSADHLVYVNSLIVNFEESQTFGLYKL 281

Db 240 HSYLGAVENTLSADHLVYVNSLIVNFEESQTFGLYKL 280

 CC RESULT 3
 CC ID TNF6_MACMU STANDARD; PRT; 280 AA.
 CC AC 09MYL6; 09BWD5;
 CC DT 15-JUN-2002 (Rel. 41, Created)
 CC DT 15-JUN-2002 (Rel. 41, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
 CC DE (CD95L protein).
 CC GN TNFRSF6 OR FASL OR CD95L.
 CC OS Macaca mulatta (Rhesus macaque),
 CC OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
 CC OS Macaca nemestrina (Pig-tailed macaque).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC OC Cercopithecoidea; Macaca.
 CC OX NCBI_TaxID-9544, 9541, 9545;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES=M.mulatta; TISSUE=Lymphocytes;
 CC RX MEDLINE-21383618; PubMed-11491535;
 CC RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 CC RA Weiss W.R., Ansari A.A.;
 CC RT "Cloning, sequencing, and homology analysis of nonhuman primate
 CC RT Fas/Fas-ligand and co-stimulatory molecules.*";
 CC RL Immunogenetics 53:315-328(2001).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
 CC RA Kiriil Y., Inoue T., Yoshino K.;
 CC RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC CC -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF8/DCR3
 CC modulates its effects (By similarity).
 CC -1- SUBUNIT: Homotrimer (Potential).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 CC similarity).
 CC -1- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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 CC EMBL: AF344847; AAK37539.1; -
 CC EMBL: AB035138; BAA90294.1; -
 CC EMBL: AB035139; BAA90295.1; -
 CC EMBL: AB035140; BAA90296.1; -
 CC HSSP: P01375; 4TSV.
 CC InterPro: IPR003636; TNF_abc.
 CC InterPro: IPR000478; TNF_family.
 CC Pfam: PF00229; TNF_1.
 CC PRINTS: PR01234; TNECROSISFCT.
 CC PRODOM: PD002012; TNF_abc; 1.
 CC SMART: SM00207; TNF_1.
 CC PROSITE: PS00251; TNF_1; 1.
 CC PROSITE: PS50049; TNF_2; 1.
 CC Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
 CC CHAIN 1 280
 CC FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 CC FT MEMBER 6, MEMBRANE FORM.

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FT CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT DOMAIN 1 80 MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT TRANSMEM 81 101 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 102 280 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 4 69 (POTENTIAL).
FT SITE 128 129 EXTRACELLULAR (POTENTIAL).
FT DISULFID 201 232 PRO-RICH.
FT CARBOHYD 183 193 POLY-PRO.
FT CARBOHYD 249 259 CLEAVAGE (BY SIMILARITY).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 280 AA: 31367 MW: 608284D61A132EB4 CRC64:

Query Match 96.5%; Score 1469.5; DB 1; Length 280;
Best Local Similarity 97.5%; Pred. No. 1,4e-93;
Matches 274; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 MOOPFNYRYPQIYWDSASSPWAPPGTVLPCTSVRRRGGRRPPPPPPPLPPPP 60
DB 1 MOOPFNYRYPQIYWDSASSPWAPPGTVLPCTSVRRRGGRRPPPPPPPLPPPP 59
DB 61 PPLPPLPPLPKRGHSTGLCLVNFVNLVALVGLGMPQLFHLQELALRESTSQ 120
DB 121 MHFASLEKQIGHSPPEPKELRKVAHLTGKSNSSMPLEMDTYGIYLSGVKKKG 180
DB 120 KHTASLEKQIGHSPPEPKELRKVAHLTGKSNSSMPLEMDTYGIYLSGVKKKG 179
QY 181 LVINETGLYFVYSKYVYFGQSCNNPLSKRYVWRNSKYPODLVMMGKMVSYCTTGQMA 240
DB 180 LVINETGLYFVYSKYVYFGQSCNNPLSKRYVWRNSKYPODLVMMGKMVSYCTTGQMA 239
QY 241 RSYLGAVNLTSAHLLYVNSLSLVNFEESOTFGLYKL 281
DB 240 HSYLGAVNLTSAHLLYVNSLSLVNFEESOTFGLYKL 280

RESULT 4
TNF6_PIG STANDARD: PRT; 282 AA.
AC Q9BEA8; Q95N10; Q95M04;
AC 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (Fas antigen
DE ligand)
GN TNFSF6 OR FASL.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
OX
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE-21322533; PubMed-11429161;
RA Muneta Y., Shimoji Y., Inumaru S., Mori Y.;
RT "Molecular cloning, characterization, and expression of porcine Fas
RT ligand (CD95 ligand).";
RT J. Interferon Cytokine Res. 21:305-312(2001).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-Guanxi bama miniature pig;
RA Zhu N., Young Y.;
RT "Molecular cloning and characterization of porcine Fas ligand cDNA.";
RN [3]
RN Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
RN SEQUENCE FROM N.A.
RC TISSUE-Lymphoid;
RA Tsuyuki S., Kono M., Bloom E.T.;
RT "Cloning and potential utility of porcine Fas ligand: overexpression

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RT In porcine cells protects them from attack by human cytolytic cells.";
RN Submitted (Jul-2001) to the EMBL/Genbank/DBJ databases.
RL [4]
RP SEQUENCE FROM N.A.
RC STRAIN-Landrace x Large Yorkshire white; TISSUE-Thymocytes;
RX PubMed-11792426;
RA Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;
RT "Porcine Fas-ligand gene: genomic sequence analysis and comparison
RT with human gene.";
RL Mol. Immunol. 38:581-586(2002).
CC -1- FUNCTION: Cytokine that binds to TNFSF6/Fas, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFSF6/Fas-mediated apoptosis may have a role in the induction of
CC peripheral tolerance. In the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/Dec3
CC modulates its effects (by similarity).
CC -1- SUBUNIT: Homotrimer (Probable).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -1- INDUCTION: By IL-18.
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AB027297; BAB40919.1; -
CC EMBL: AY033634; AAK56449.1; -
CC EMBL: AF9397407; AAK84408.1; -
CC EMBL: AB069764; BAB64291.1; -
CC HSSP: P01375; 4TSV.
CC InterPro: IPR003636; TNF_abc.
CC InterPro: IPR000478; TNF_family.
CC Pfam: PF00229; TNF; 1.
CC PRINTS: PRO1234; TNFECROSISFCT.
CC ProDom: PD002012; TNF_abc; 1.
CC SMART: SM00207; TNF; 1.
CC PROSITE: PS00251; TNF_1; 1.
CC PROSITE: PS0049; TNF_2; 1.
CC Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 282
FT CHAIN 131 282
FT DOMAIN 1 82
FT TRANSMEM 83 103
FT DOMAIN 104 282
FT DOMAIN 4 70
FT SITE 130 131
FT DISULFID 203 234
FT CARBOHYD 185 185
FT CARBOHYD 251 251
FT CARBOHYD 261 261
FT CONFLICT 5 5
FT CONFLICT 57 57
SQ SEQUENCE 282 AA: 31756 MW: 6743DA1145671FB CRC64:

Query Match 85.1%; Score 1295.5; DB 1; Length 282;
Best Local Similarity 85.5%; Pred. No. 9,8e-82;
Matches 242; Conservative 14; Mismatches 24; Indels 3; Gaps 2;

QY 1 MOOPFNYRYPQIYWDSASSPWAPPGTVLPCTSVRRRGGRRPPPPPPPLPPPP 58
DB 1 MOOPFNYRYPQIYWDSASSPWAPPGTVLPCTSVRRRGGRRPPPPPPPLPPPP 59

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FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 210 MISSING (IN ISOFORM FASLS).
 FT VARIANT 184 184 T -> A (IN STRAINS BAB/C AND DBA;
 FT VARIANT 218 218 ENHANCES CYTOTOXICITY).
 FT VARIANT 218 218 E -> G (IN STRAINS BAB/C AND DBA;
 FT VARIANT 273 273 ENHANCES CYTOTOXICITY).
 FT VARIANT 273 273 F -> L (IN GLD: ABOLISHES BINDING OF FASL
 TO ITS RECEPTOR).
 SQ SEQUENCE 279 AA: 31442 MW: 37972E2728E0A1CA CRC64;

Query Match 75.9%; Score 1156; DB 1; Length 279;
 Best Local Similarity 77.3%; Pred. No. 3.1e-72;
 Matches 218; Conservative 25; Mismatches 35; Indels 4; Gaps 3;

QY 1 MOQFNYPPQIYWDSSASSPAPPGTVLPCTSVPRRGGRRPPPPPP-PLPPLPPP 59
 DB 1 MOQPMVPCQIYWDSSASSPAPPGTVLPCTSVPRRGGRRPPPPPP-PLPPLPPP 60
 QY 60 PPLPLPLPLPLPKKRGHNSGTGLVMEFVAVLALVGLGMQLFHLQKELAELEST 119
 DB 61 PLPLP--PLPLPKK--DHNTNMLPVYFVAVLALVGLGMQLFHLQKELAELEST 117
 DB 120 QMHTASSLEKQIGHPSPPEKKELRYVAHLTGKSNRSMPLMEDTYGIVLLSGVYKKG 179
 QY 118 QSLKVSFSEKQIANPSTPSEKPRSAVHLTGKSNRSMPLMEDTYGIVLLSGVYKKG 177
 DB 180 GLVINTETGLYFYSKYFPGQSCNPLPLSHKYVNRSKYPODLYMMEGKMSCTTGQW 239
 DB 178 GLVINTETGLYFYSKYFPGQSCNPLPLSHKYVNRSKYPODLYMMEGKMSCTTGQW 237
 QY 240 ARSSYLGAVERNLSADHLVYVNSLIVNEESQTFEGLYKL 281
 DB 238 AHSSYLGAVERNLSADHLVYVNSLIVNEESQTFEGLYKL 279

RESULT 6
 TNF6_RAT
 ID TNF6_RAT STANDARD; PRT: 278 AA.

AC P36940;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand).
 GN TNFSF6 OR FASL OR APRILG.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 NCBI_TaxID=10116;

SEQUENCE FROM N.A.
 MEDLINE=94084792; PubMed=7505205;

RA Suda T., Takahashi T., Golstein P., Nagata S.;
 RT "Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor family.";
 RL Cell 75:1169-1178(1993).

CC -1- FUNCTION: Cytokine that binds to TNFSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/Decr3 modulates its effects (By similarity).
 CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES, KIDNEY AND LUNG.
 CC -1- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
 CC -1- PTM: The soluble form derives from the membrane form by

CC proteolytic processing (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 CC -----

DR EMBL: U03470; AAC52129.1; -
 DR HSSP: P01375; 4TSV.
 DR InterPro: IPR003636; TNF_ab.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF_1.
 DR ProDom: PD002012; TNF_ab; 1.
 DR SMART: SM00207; TNF_1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 278 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT DOMAIN 127 278 MEMBER 6, MEMBRANE FORM.
 FT DOMAIN 1 77 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT TRANSMEM 78 99 CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT PRO-RICH.
 FT POLY-PRO.
 FT CLEAVAGE (BY SIMILARITY).
 FT SITE 126 127 POTENTIAL.
 FT DISULFID 199 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 278 AA: 31140 MW: 289818A862CEAC6 CRC64;

Query Match 74.6%; Score 1136.5; DB 1; Length 278;
 Best Local Similarity 76.6%; Pred. No. 6.6e-71;
 Matches 216; Conservative 21; Mismatches 40; Indels 5; Gaps 3;

QY 1 MOQFNYPPQIYWDSSASSPAPPGTVLPCTSVPRRGGRRPPPPPP-PLPPLPPP 59
 DB 1 MOQPMVPCQIYWDSSASSPAPPGTVLPCTSVPRRGGRRPPPPPP-PLPPLPPP 60
 QY 60 PPLPLPLPLPLPKKRGHNSGTGLVMEFVAVLALVGLGMQLFHLQKELAELEST 119
 DB 61 PLPLP--PLPLPKK--DHNTNMLPVYFVAVLALVGLGMQLFHLQKELAELEST 117
 DB 120 QMHTASSLEKQIGHPSPPEKKELRYVAHLTGKSNRSMPLMEDTYGIVLLSGVYKKG 179
 QY 118 QSLKVSFSEKQIANPSTPSEKPRSAVHLTGKSNRSMPLMEDTYGIVLLSGVYKKG 177
 DB 178 GLVINTETGLYFYSKYFPGQSCNPLPLSHKYVNRSKYPODLYMMEGKMSCTTGQW 239
 DB 177 GLVINTETGLYFYSKYFPGQSCNPLPLSHKYVNRSKYPODLYMMEGKMSCTTGQW 236
 QY 240 ARSSYLGAVERNLSADHLVYVNSLIVNEESQTFEGLYKL 281
 DB 237 AHSSYLGAVERNLSADHLVYVNSLIVNEESQTFEGLYKL 278

RESULT 7

TN14_MOUSE
 ID TN14_MOUSE STANDARD; PRT: 239 AA.

AC O90YH9;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 14.
 GN TNFSF14 OR LIGHT.
 OS Mus musculus (Mouse).

OY		68	LPLPKRKNHSTGCLLMEFMAVLAVGLG---	GHEOLFHLQKEIAEL-----RE	116
Dd		18	IPFRLEGNHHRRRCGGIVQVSLAVLLGSLAQGW-	LRLNORGLGDIVAHLPDGGKG	76
OY		117	STSQMHTASSLEKIOIGHPSPPEKKELKVAAHLTKRSNR--	SMPLEWEDTVGIALLSG	173
Dd		77	SMERL-----IQDORSHOANP-----	AAHLTGAMNAASLTIGIGCPLIMETRIAGLATLRG	123
OY		174	VKKYKGGVINEITGLTFPYYSKYVYRGSC-----	NNPLSKIVYMRSKYPQDYVMNEKG	228
Dd		124	LTYHDGALVTMEPEYYYSKVSQOLSGVGCPOGLANGLPETHGLVKRTSRYPKELELLVSR	183	
OY		229	MMSYC---TTGOMARSSYLCAVENLTSADILYNVSELSVFNEE-SOFFFGLY	279	
Dd		184	-RSPCGGRANSRVMMWDSFLGGVYHLEAGEVYVRVIGNRLVPRDRGTSTFGAF	237	
 RESULT 8 TN14_HUMAN					
ID	TN14_HUMAN	STANDARD:	PRT:	240 AA.	
AC	043557,	G75A476; Q96ID2; Q8WVE;			
DI	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry mediator-ligand) (HVEM-L).				
CN	TNFSF14 OR LIGHT OR HVEM-L.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
OX	NCBI_Taxid=9606;				
RP	[1]				
RN	SEQUENCE FROM N.A. (ISOFORM 1).				
EX	MEDLINE=96122340; PubMed=9462508;				
RA	Maui D.N., Ebner R., Montgomery J.T., Kochel K.D., Cheung T.C.,				
RA	Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,				
RA	Ware C.F.;				
RT	"LIGHT", a new member of the TNF superfamily, and lymphotoxin alpha are				
RT	ligands for herpesvirus entry mediator.";				
RL	Immunity 8:21-30(1998).				
RL	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.				
RC	TISSUE=Liver;				
RC	MEDLINE=98438532; PubMed=9765287;				
RX	Harrop J.A., McDonnell P.C., Brihan-Burke M., Lyn S.D., Minton J.,				
RA	Tan K.B., Dece K., Spanpanato J., Silverman C., Hensley P.,				
RA	DiPrinzio R.I., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,				
RA	Tunneh A., Young P.R.;				
RT	"Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for				
RT	HVEM/RL2, stimulates proliferation of T cells and inhibits HT29 cell				
RT	growth".				
RL	J. Biol. Chem. 273:27548-27556(1998).				
RL	[3]				
RN	SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.				
RP	MEDLINE=21528948; PubMed=11673523;				
RA	Granger S.W., Butrovich K.D., Houshand P., Edwards W.R., Ware C.F.;				
RT	"Genomic characterization of LIGHT reveals linkage to an immune				
RT	response locus on chromosome 19p13.3 and distinct isoforms generated				
RT	by alternate splicing or proteolysis."				
RL	J. Immunol. 167:5122-5128(2001).				
RL	[4]				
RP	SEQUENCE FROM N.A.				
RP	TISSUE=Brain;				
RA	Strassburg R.C.				
CC	Submitted (Dec-2001) to the EMBL/GenBank/DDBJ databases.				
CC	-I- FUNCTION: Cytokine that binds to TNFRSF3/LTRB. Binding to the				
CC	decoy receptor TNFRSF6B modulates its effects. Activates NFkB,				
CC	stimulates the proliferation of T cells, and inhibits growth of				
CC	the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex				
CC	virus.				
-I-	SUBUNIT: Homotrimer.				
-I-	SUBCELLULAR LOCATION: Type II membrane protein and secreted				

DB 108 SOVVFSGESCSRAIPPTPIYLAHEVOLFFSSQYPPFVPLLSAOKSVYFGLOGPVMWSMYOG 167
 QY 247 AVFNLTSAADHLVYVNSLNVNEESQTFEGLYKL 281
 DB 168 AVFLLSKGDLSTHTDGLSHLHSPSVYFFGAFAL 202

RESULT 10
 TNFB_MOUSE
 ID TNFB_MOUSE STANDARD: PRT: 202 AA.
 AC P09225;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis factor ligand superfamily member 1).
 LTR OR TNFSF1 OR TNFB.
 Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88067722; PubMed-3684584;
 RA Semon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;
 RT "Nucleotide sequence of the murine TNF locus, including the TNF-alpha (tumor necrosis factor) and TNF-beta (Lymphotoxin) genes.";
 RL Nucleic Acids Res. 15:9083-9084(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87040736; PubMed-3490653;
 RA Nedospasov S.A., Hirt B., Shakhov A.N., Dobrynin V.N., Kawashima E.,
 RT Accolla R.S., Jongeneel C.V.;
 RL "The genes for tumor necrosis factor (TNF-alpha) and Lymphotoxin (TNF-beta) are tandemly arranged on chromosome 17 of the mouse.";
 RL Nucleic Acids Res. 14:7713-7725(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87231097; PubMed-3588316;
 RA Gray P.W., Chen E., Tang W.-L., Ruddle N.;
 RT "The murine tumor necrosis factor-beta (Lymphotoxin) gene sequence.";
 RL Nucleic Acids Res. 15:3937-3937(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87224127; PubMed-2884262;
 RA Li C.B., Gray P.W., Lin P.F., McGrath K.M., Ruddle F.H.;
 RT "Cloning and expression of murine Lymphotoxin cDNA.";
 RL J. Immunol. 138:4496-4501(1987).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87252204; PubMed-2885372;
 RA Gardner S.M., Mock B.A., Hilgers J., Huppi K.E., Roeder W.D.;
 RT "Mouse Lymphotoxin and tumor necrosis factor: structural analysis of the cloned genes, physical linkage, and chromosomal position.";
 RL J. Immunol. 139:476-483(1987).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Rowen L., Qin S., Madan A., Abbasi N., James R., Dickhoff R.,
 RA Shafer T., Ratcliffe A., Loretz C., Lasky S., Hood L.;
 RT "Sequence of the mouse major histocompatibility class III region.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 6-202 FROM N.A.
 RX MEDLINE-89144562; PubMed-3147435;
 RA Weill D., Dautry F.;
 RT "Induction of tumor necrosis factor-alpha and -beta and interferon-gamma mRNA by Interleukin 2 in murine lymphocytic cell lines.";
 RL Oncogene Res. 3:409-414(1988).
 RN [8]
 RP SEQUENCE OF 56-76 FROM N.A.
 RX MEDLINE-91042516; PubMed-1700275;

RA Weill D., Brosset S., Dautry F.;
 RT "RNA processing is a limiting step for murine tumor necrosis factor beta expression in response to Interleukin-2.";
 RL Mol. Cell. Biol. 10:5865-5873(1990).
 CC -1- FUNCTION: Cytokine that in its homotrimeric form binds to TNFRSF1A/TNFR1, TNFRSF1B/TNFR and TNFRSF14/HVEM. In its heterotrimeric form with LTB binds to TNFRSF3/LTR. Lymphotoxin is produced by lymphocytes and cytotoxic for a wide range of tumor cells in vitro and in vivo.
 CC -1- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one LTA subunits or (less prevalent) two LTA and one LTB subunits (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane protein (heterotrimers) (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
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 CC
 DR EMBL: U06950; AAA18593.1; -;
 DR EMBL: Y00467; CAAG8529.1; -;
 DR EMBL: X06217; CAA29566.1; -;
 DR EMBL: X06218; CAA29567.1; -;
 DR EMBL: Y00137; CAA68330.1; -;
 DR EMBL: M16819; AAA40460.1; -;
 DR EMBL: M17015; AAA39450.1; -;
 DR EMBL: AF109719; AAC82485.1; -;
 DR EMBL: X14800; CAA32906.1; -;
 DR EMBL: M60586; AAA40461.1; -;
 DR PIR: B27303; B27303.
 DR PIR: S01342; S01342.
 DR HSSP: P01374; 1TNR.
 DR MGD: MGI:104797; Lta.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF_1.
 DR PRINTS: PR01234; TNCRSISFCT.
 DR ProDom: PD002012; TNF_abc; 1.
 DR SMART: SM00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR PROSITE: PS500251; TNF_1; 1.
 KW Cytokine; Glycoprotein; Cytotoxin; Signal.
 FT SIGNAL 1 33
 FT CHAIN 34 202 LYMPHOTOXIN-ALPHA.
 FT CARBOHYD 94 94 N-LINKED (GLCNAC...)
 FT CONFLICT 26 26 A->P (IN REF. 5).
 FT CONFLICT 161 162 VR->CG (IN REF. 2).
 SO SEQUENCE 202 AA; 21998 MW; F496FB3C685950D3 CRC64;

Query Match 13.4%; Score 204; DB 1; Length 202;
 Best Local Similarity 32.5%; Pred. No. 1.7e-07;
 Matches 51; Conservative 25; Mismatches 73; Indels 8; Gaps 2;

QY 133 HPSPPPEKKE--LRKVAHLTKRSNSRMPLEMDTYGIVLLGYKRYKGGIVINETGLYF 190
 DB 46 HPLPQKHLTHGILKPAHLVGVPSKQNSLWRASPDRAFLHFGSLSNNSLLIPTSGLYF 105
 QY 191 VYSKYVYFRGQSCN-----NPLSHKYVMRSKPKIPQDLYVMEGKMSYCTTGQMMANSY 244
 DB 106 VYSQVVFSGESCSRAIPPTPIYLAHEVOLFFSSQYPPFVPLLSAOKSVYFGLOGPVMWSMY 165
 QY 245 LGAVFNLTSAADHLVYVNSLNVNEESQTFEGLYKL 281
 DB 166 OGAVFLLSKGDLSTHTDGLSHLHSPSVYFFGAFAL 202

RESULT 11


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Db      42  POTAQHL$OKSLKRETLKPAHVLGDP$VOD-SIHWRANTHAFLRHGFSL$NN$SLVPT 100
Qy      186 TGLFYVSKYFYRQSCNN-----LPISHKYMRNSKYPODLYMNEGKMSYCTTGQWMA 240
Db      101 SGLFYV$QVFFS$SCSEIPTLLYLSHEVLFF$SKQVYVPL$S$QK$V$C$G$T$G$P$W$M 160
Qy      241 R$SYGAVFNLTSADHLYVNVSELSLVNFEE$Q$T$F$GLYKL 281
Db      161 R$SYGAVFNLTOGDR$LT$YTD$V$SHLQ$P$S$V$F$F$G$F$AL 201

RESULT 13
TN10_MOUSE STANDARD: PRT: 291 AA.
AC P50592:
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
  apoptosis inducing ligand) (TRAIL protein).
GN TNFSF10 OR TRAIL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96111955; PubMed=8777713;
RA Willey S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholson J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF
  family that induces apoptosis."
RL Immunity 3:673-682(1995).
CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
  TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
  possibly also to TNFRSF1B/OPG. Induces apoptosis. Its activity
  may be modulated by binding to the decoy receptors
  TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF1B/OPG that cannot
  induce apoptosis.
CC -1- SUBUNIT: HOMOTRIMER (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (potential).
CC -1- TISSUE SPECIFICITY: WIDESPREAD.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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  entities requires a license agreement (see http://www.isb-sib.ch/announce/
  or send an email to license@sib-sib.ch).
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DR EMBL; U37522; AAC52345.1; -
DR HSSP; P50591; IDOG.
DR MGD; MGI:107414; Tnfsf10.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR00478; TNF_Family.
DR Pfam; PF00229; TNF_1.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS00251; TNF_1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Signal-anchor; Apoptosis.
FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
  (POTENTIAL).
FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 52 52 N-LINKED (GLCNAc...) (POTENTIAL).
SO SEQUENCE 291 AA; 33477 MW; 3FEACB9F0D7D802 CRC64;
Query Match 13.2%; Score 200.5; DB 1; Length 291;

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```

Best Local Similarity 28.3%; Pred. No. 4.2e-07;
Matches 60; Conservative 39; Mismatches 68; Indels 45; Gaps 9;

Qy      103 QLFHLQKLAELRESTSQMHTASSLEKQIGHSPPEPKELRKVAHLTG---KNSR$MP 159
Db      87 QLYQLEI$VT-LR--TFQDIT$TVEKOL$P$P$P$R$G$R$P$K$V$A$H$T$G$T$R$R$S$A$LP 143
Qy      160 L-----EMEDT-YGIVLL$G$V$K$K$G$V$IN$ET$G$LY$F$Y$K$V$Y$F$R$G$SC$N$NL- 205
Db      144 I$K$Q$K$T$G$Q$K$IES$E$S$R$K$H$P$LN$H$V$L$F$R$N$G$E$LY$I$Q$E$G$LY$I$Y$S$Q$T$Y$R$F$Q$E$A$D$A$S 203
Qy      206 -----PL$H$K$Y$M$R$N$S$K$Y$P$O$D$LY$M$N$E$G$K$M$S$Y$C$T$G$Q$W$M$A$-----S$Y$Y$G$A 247
Db      204 K$W$S$K$D$K$V$T$K$Q$V$Q$Y$I-K$Y$T$S$Y$D$P$IV$L$K$M$K$A$R$N$S-----C$M$S$R$D$A$E$G$LY$S$Y$G$G 256
Qy      248 V$N$T$S$A$D$H$LY$V$N$S$E$LS$V$N$F$E$S$Q$T$F$G$LY 279
Db      257 L$F$E$L$K$N$D$R$I$V$S$Y$V$N$E$H$L$M$D$D$E$A$S$F$F$G$A$F 288

RESULT 14
TNFB_RABIT STANDARD: PRT: 197 AA.
AC P10154;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
  factor ligand superfamily member 1).
GN LTA OR TNFSF1 OR TNFB.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91065534; PubMed=2249779;
RA Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,
RA Andreyeva A.V., Nedospasov S.A.;
RT "Cloning and structural analysis of genes coding for tumor necrosis
  factor and lymphotoxin in rabbits."
RL Mol. Biol. (Mosk) 23:1743-1750(1989).
CC -1- FUNCTION: Cytokine that in its homotrimeric form binds to
  TNFRSF1A/TNFR1, TNFRSF1B/TNFR and TNFRSF3/LTBR. Lymphotoxin is
  produced by lymphocytes and cytotoxic for a wide range of tumor
  cells in vitro and in vivo.
CC -1- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
  LTA subunits or (less prevalent) two LTA and one LTB subunits (By
  similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane
  protein (heterotrimers) (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
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  or send an email to license@sib-sib.ch).
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DR EMBL; X55745; CAA39275.1; ALT_SEQ.
DR EMBL; M60340; AAA31483.1; -

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DR EMBL: M60341; AAA31485.1; -
DR PIR: JH0309; JH0309.
DR PIR: P00098; P00098.
DR HSSP: P01374; 1TNR.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS00049; TNF_2; 1.
DR CytoKine: Glycoprotein; Cytotoxin; Signal.
KW SIGNAL
FT CHAIN 1 26 LYMPHOTOXIN-ALPHA.
FT CARBOHYD 88 88 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 197 AA; 21126 MW; 0CF18CC90B5E2345 CRC64;

Query Match 13.18; Score 200; DB 1; Length 197;
Best Local Similarity 26.0%; Pred. No. 3e-07;
Matches 61; Conservative 28; Mismatches 82; Indels 64; Gaps 7;

55 PPPPPPLPLPLPLKRGKNGSTGCLLVMEFVVALVGLGMFLHQLKELAE 114
19 PPPPGAGLPAGAFPPSAAR----- 38
115 RESTSQMHTASSLEKQIGHPSPPEKELKVAHLTGKNSRSMPLWE-DYGIYLLSG 173
39 -----NAQQRLOKHFGHST-----LKPAHLVGDPSAD-SLRMRNTRAPFLRHG 83
174 VKKKGGVYINENGLFYYSKYFRGOSCN-----NLPLSHVYMRNSYPPDLYMEG 227
84 FSLSNSLLVPSGGLFYVSQVSESGSPKAVPPPLLAHVQVLFSSQYSHVPLLSA 143
228 KMSYCTTGO-MMARSSYLGAVENTSADHLVYNSELVNFEEOSTFGYIKL 281
144 Q-KSVCPGPGVNRSVYOGAVFLITGQDLSTHTGIAHLILSPSVFFGAPAL 197

RESULT 15
TN15_HUMAN
ID TN15_HUMAN STANDARD; PRT; 174 AA.
AC 095150;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor ligand superfamily member 15 (Vascular
endothelial cell growth inhibitor) (TNF ligand-related molecule 1).
GN TNFSF15 OR VEGI OR TLI.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=umbilical vein;
RX PubMed=9872942;
RA Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,
Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S.,
Li L.-Y., Gentz R., Yu G.-L.;
RA "VEGI, a novel cytokine of the tumor necrosis factor family, is an
RT angiogenesis inhibitor that suppresses the growth of colon carcinomas
in vivo."
RT FASEB J. 13:181-189(1999).
RL
CC -1- FUNCTION: Inhibits vascular endothelial growth and angiogenesis
(in vitro).
CC -1- SUBUNIT: Homotrimer (Potential).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.
CC Detected in placenta, lung, kidney, skeletal muscle, pancreas,
CC spleen, prostate, small intestine and colon.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC or send an email to license@isb-sib.ch).

DR EMBL: AF039390; AAD08783.1; -
DR Genew: HGNC:11931; TNFSF15.
DR MIM: 604052; -
DR HSSP: P50591; 1DOC.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00049; TNF_2; 1.
DR CytoKine: Transmembrane; Glycoprotein; Signal-anchor.
KW DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 26 174 EXTRACELLULAR (POTENTIAL).
FT DISULFID 85 125 POTENTIAL.
FT CARBOHYD 56 56 N-LINKED (GLCNAC...) (POTENTIAL).
FT FT 152 152 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 174 AA; 20131 MW; CCB83BA7EE673B98 CRC64;

Query Match 12.78; Score 193.5; DB 1; Length 174;
Best Local Similarity 36.88; Pred. No. 7.4e-07;
Matches 50; Conservative 22; Mismatches 49; Indels 15; Gaps 6;

160 LEMEDFYGIYLLSG-VKKKGGVYINENGLFYYSKYFRGOS--CN-----NLPLS 208
40 LHMHEHGLAFTNRRNNTNKKLLIPESGDYFIYSQVTRGKMTSECSLROGRPKPPS 99
209 HKVYNR-NSKYPQDLVMEGKMSYCTTGQMARSSYLGAVENTSADHLVYNSEL 266
100 IFVIVITKVTDSYDEPQLLMG-TKSVCEVGSNMFQPIYLGAMFSLQEGDKLWVNSDISL 158
267 VNF-EESQTFEYIKL 281
159 VDYTKEDKTFEGFALL 174

Search completed: June 24, 2003, 11:05:28
Job time : 11.364 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2003, 11:01:33 ; Search time 21.3505 Seconds

(Without alignments)
1265.253 Million cell updates/sec

Title: US-09-508-849a-17

Perfect score: 1523

Sequence: 1 MQDPFNYPYQIYWDSAS.....SELSLVNFEESQPFGLYKL 281

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
5: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1523	100.0	281	2	I38707 Fas ligand - human
2	1156	75.9	279	2	A53062 Fas ligand - mouse
3	1136.5	74.6	278	2	A49266 fas ligand - rat
4	205	13.5	202	1	JN0869 tumor necrosis fac
5	204	13.4	202	1	B27303 tumor necrosis fac
6	200	13.1	197	1	JH0309 tumor necrosis fac
7	191	12.5	205	1	OMH0X lymphotoxin alpha
8	186.5	12.2	234	1	JO1344 tumor necrosis fac
9	185.5	12.2	232	1	S12606 tumor necrosis fac
10	184	12.1	204	1	SI7289 tumor necrosis fac
11	183.5	12.0	204	1	S24642 lymphotoxin - bovi
12	183	12.0	233	1	S47642 tumor necrosis fac
13	181	11.9	233	1	OMHUN tumor necrosis fac
14	177	11.6	141	2	A34043 hypothetical proli
15	176	11.6	233	1	S2202 tumor necrosis fac
16	175	11.5	234	1	A25451 tumor necrosis fac
17	172	11.3	599	2	T10798 pterophorin-S - Vo
18	171.5	11.3	415	1	A34170 acrostin (EC 3.4.21
19	169.5	11.1	185	2	S52715 tumor necrosis fac
20	169.5	11.1	485	2	A33647 sulfated surface g
21	165.5	10.9	389	2	S17200 prolina-rich prote
22	165	10.8	233	2	SI1668 tumor necrosis fac
23	163.5	10.7	234	1	JH0529 tumor necrosis fac
24	163	10.7	431	2	S47538 acrostin (EC 3.4.21
25	162.5	10.7	1206	2	S24407 formin isoform IV
26	162.5	10.7	1468	2	SI1515 formin - mouse
27	161	10.6	193	2	S06132 tumor necrosis fac
28	160	10.5	235	2	SI5490 tumor necrosis fac
29	159.5	10.5	421	1	SI1674 acrostin (EC 3.4.21

30	158.5	10.4	502	2	A55197
31	157	10.3	235	1	OMMSN
32	155.5	10.2	306	2	I49139
33	155.5	10.2	440	2	I49681
34	154	10.1	235	2	JU0029
35	153	10.0	708	2	D96711
36	153	10.0	760	2	T06291
37	152.5	10.0	1110	2	T19673
38	152	10.0	487	2	S42442
39	151	9.9	196	2	B48232
40	151	9.9	439	2	S51939
41	151	9.9	980	2	S54986
42	151	9.9	1201	2	G86441
43	150.5	9.9	464	2	S22697
44	150.5	9.9	1255	2	T31065
45	149.5	9.8	645	2	A71416

ALIGNMENTS

RESULT 1

I38707 Fas ligand - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: I38707; JG2340; S57565; I38554

R:Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.

Int. Immunol. 6, 1567-1574, 1994

A:Title: Human Fas ligand: gene structure, chromosomal location and species specificity

A:Reference number: I38707; MUID:95127560; PMID:7826947

A:Accession: I38707

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-281 <RES>

A:Cross-references: EMBL:U11821; NID:9595430; PIDN:AAC50124.1; PID:9595431

R:Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, B.

Biochem. Biophys. Res. Commun. 204, 468-474, 1994

A:Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.

A:Reference number: JG2340; MUID:95071350; PMID:7980502

A:Accession: JG2340

A:Molecule type: DNA

A:Residues: 1-281 <MIT>

A:Cross-references: GB:D38122; DDBJ:D29820; NID:9601892; PIDN:BA07320.1; PID:9136990

R:Schatzlein, C.E.

Submitted to the EMBL Data Library, June 1995

A:Reference number: S57565

A:Accession: S57565

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-281 <SCH>

A:Cross-references: EMBL:X89102; NID:9687455; PID:9687456

R:Riderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.;

J. Exp. Med. 181, 71-77, 1995

A:Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.

A:Reference number: I38554; MUID:95105731; PMID:7528780

A:Accession: I38554

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-281 <RE2>

A:Cross-references: EMBL:U08137; NID:9624627; PIDN:AAC50071.1; PID:9624628

C:Genetics:

A:Gene: FasL

A:Introns: 151/1; 116/3

C:Keywords: glycoprotein; transmembrane protein.

F:80-102/Domain: transmembrane #status predicted <TM>

F:76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0% Score 1523 DB 2 Length 281;
Best Local Similarity 100.0% Pred. No. 1.2e-104;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MQDPFNYPYQIYWDSASSPMAPGTVLPCPTSVPRRCQRRPPPPPPPLPPPPP 60

[illegible]

RESULT 2
A53062
Ligand - mouse
Species: Mus musculus (house mouse)
Create: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
Accession: A53062
R: Takahashi, T.; Tanaka, M.; Brennan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Naei
Cell 76. 969-976, 1994
A: Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A: Reference number: A53062; MUID:94185175; PMID:7511063
A: Accession: A53062
A: Status: Preliminary
A: Molecule type: mRNA
A: Residues: 1-279 <TAK>
A: Cross-references: GB:006948; NID:9473564; PIDN:AAA17800.1; PID:9473565

Query Match	75.9%	Score 1156;	DB 2;	length 279;
Best Local Similarity	77.3%	Pred. No. 1e-77;		
Matches	218;	Conservative	25;	Mismatches 35; Indels 4; Gaps 3
Qy	1	MOQFNPYPIQIYWDSSASSBP	PGTVLP	CPISVPRRPGORRPPPPP-PPLP
Db	1	MQQMNPPCPDIFWDDSSATSM	APGCVFPC	PGSCGPGPDRRPPPPPPSP
Qy	60	PPPLPPLPPLPKKRGHNSTG	LCILVMEFNV	VALVAGLGMLQFHLQKELAE
Db	61	PLPLP-PLPLPKK-K	DHNTLM	LPYVEFNVVALVAGLGMLQFHLQKELAE
Qy	120	QMHTASSLEKQIGHPSPPE	KKELAKVA	HLTGKSNSRMPLEMDTYGIVL
Db	118	QSLKVSSEFKQIAPSTPSE	KKERPSVA	NHLGPNPSRRIPLMEMDTYGIVL
Qy	180	GLVINEGLGVVYSKYVYFG	QSCNNLPL	PSHYVYMNRSKYPDOLIVAEK
Db	178	GLVINEGLGVVYSKYVYFG	QSCNNQPL	NHRVYMNRSKYPEDIVIMEKRL
Qy	240	ARSSYLGAVRLTSSADHL	VYVASELS	LVNFEESQTFGLYKL
Db	238	AHSSTLGAVENTLTSSADH	LYVNIQS	LTINFEESKTFGLYKL

RESULT 3
A49266
fas ligand - rat
C,Species: Rattus norvegicus (Norway rat)
C,Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C,Accession: A49266
R,Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A,Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor
A,Reference number: A49266; MUID:94084792; PMID:7505205
A,Accession: A49266
A,Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-278 <SUD>
A:Cross-references: GB:003470; NID:G440178; PIDN:AAC52129.1; PID:G440179
C:Keywords: glycoprotein; transmembrane protein

Query Match	74.68	Score 1136.5	DB 2	Length 278
Best Local Similarity	76.68	Pred. No. 2.8e-76		
Matches 216	Conservative 21	Mismatches 40	Indels 5	Gaps 3

```

QY 1 MOOPFNXPYQIOWDSSSSPMAPPGVLTCPSTVPPRRGRRRPPPP - PLPPPP 59
QY 2 MOOPFNXPYQIOWDSSSSPMAPPGVLTCPSTVPPRRGRRRPPPP - PLPPPP 60
Db 1 MOQPVNXPQIOWDSSATSPMAPPGVSFCSSSGPQGGRRRPPPPPPPLPPSQ 60
QY 60 PPLPLPPLPLPKKKRNNHSTGCLVMPFMVLYALVGLGMLFQHLQKELARESTS 119
QY 61 PPLPLP - PLSPLEKKKN - IELMLPPIEFMMVYALVGLGMLYQFLQKELARET 116
Db 120 QMHTASSLEKQICHPSPPEKKELRLVAHTGCSNRSRMPLEMETTYGIVLSCVKKKG 179
Db 117 HSLRVSSFEKQIANPSTPSETKPKPSVAHLTNPNRSRSLPLEMETTYGIVLSCVKKKG 178
QY 180 GLVINEETGLYFYVSKYVFRGQSCNNLPLSHKYVMNSKYYPODLYAMEGKMSYCTTGOM 235
QY 177 GLVINEAGLYFYVSKYVFRGQSCNSOPLSHKYVMNFKYPGDIYVLEKKRLNYCTTGQIW 236
Db 240 ARSSYLGAVPNLTADHLVYVNSSELINVEESORFFGLYTK 281
Db 237 AHSSYLGAVPNLTADHLVYVNSQSLINVEESKFFFGYTK 278

```

RESULT 4
JN0869
tumor necrosis factor beta - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text-change 10-Sep-1999
C:Accession: JN0869
R:Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A:Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding gene
A:Reference number: JN0868; MUID:34040766; PMID:8224868
A:Accession: JN0869
A:Molecule type: DNA
A:Residues: 1-202 <RWO>
A:Cross-references: GB:U00981; NID:g205253; PIDN:AAA16276.1; PID:g205255
A:Note: the authors translated codon CTC for residue 172 as Ile
C:Comment: This protein is structurally related pleiotropic cytokinase with overlappl
C:Geneids:
A:Gene: TNF-beta
A:Introns: 32/3; 66/1
C:Superfamily: tumor necrosis factor
;Keywords: tumor

[illegible]

RESULT 5
B27303
tumor necrosis factor beta precursor - mouse
N:Alternate names: Lymphotoxin; TNF beta

C:Species: Mus musculus (house mouse)
C:date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
C:Accession: B27303; S0142; S10083; I56004; I48853; I55960
R:Simon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A>Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor necrosis factor)-beta gene
A:Reference number: A93679; MUID:88067722; PMID:3684584
A:Accession: B27303
Molecule type: DNA
A:Residues: 1-202 <SEN>
A:Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68529.1; PID:g54831
R:Nedospasov, S.A.; Hlry, B.; Shakhov, A.N.; Dobrynin, V.N.; Kawashima, E.; Accolla, R.S.
Nucleic Acids Res. 14, 7713-7725, 1986
A>Title: The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) are located at the same chromosomal position as the TNF gene
A:Reference number: S01342; MUID:87040736; PMID:3450653
A:Accession: S01342
Molecule type: DNA
A:Residues: 1-11;139-160,'CG','163-178 <NED>
A:Cross-references: EMBL:X06217
R:Well, D.; Dautry, F.
Oncogene Res. 3, 409-414, 1988
A>Title: Induction of tumor necrosis factor-alpha and -beta and interferon-gamma mRNA by lipopolysaccharide in macrophages
A:Reference number: S10083; MUID:89144562; PMID:3147435
A:Accession: S10083
Molecule type: mRNA
A:Residues: 6-202 <NEI>
A:Cross-references: EMBL:X14800; NID:g54833; PIDN:CAA32906.1; PID:g736269
R:Gardner, S.M.; Mock, B.A.; Hligers, J.; Hunpl, K.E.; Roeder, W.D.
J. Immunol. 139, 476-483, 1987
A>Title: Mouse lymphotoxin and tumor necrosis factor: Structural analysis of the cloned cDNAs
A:Reference number: I56004; MUID:87252204; PMID:2885372
A:Accession: I56004
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
A:Residues: 1-25,'P',27-202 <RES>
A:Cross-references: GB:M17015; NID:g198880; PIDN:AAA39450.1; PID:g387407
R:Gray, P.W.; Chen, E.; Li, C.B.; Tang, W.L.; Ruddie, N.
Nucleic Acids Res. 15, 3937, 1987
A>Title: The murine tumor necrosis factor-beta (lymphotoxin) gene sequence.
A:Reference number: I48853; MUID:87231097; PMID:3588316
A:Accession: I48853
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
A:Residues: 1-202 <RE2>
A:Cross-references: EMBL:Y00137; NID:g54842; PIDN:CAA68330.1; PID:g54843
R:
Immunol. 138, 4496-4501, 1987
A>Title: Cloning and expression of murine lymphotoxin cDNA.
A:Reference number: I55960; MUID:87224127; PMID:2884262
A:Accession: I55960
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
A:Residues: 1-202 <REA>
A:Cross-references: GB:M16819; NID:g202088; PIDN:AAA0460.1; PID:g202089
Comment: The first intron occurs in the 5'-untranslated region.
Genetics:
Gene: Tnfr
Map position: 17
Introns: 32/3; 66/1
Superfamily: tumor necrosis factor
Keywords: cytokine; cytotoxicity; glycoprotein; lymphokine; macrophage

Query Match 13.4%; Score 204; DB 1; Length 202;
Best Local Similarity 32.5%; Pred. No. 5e-08;
Matches 51; Conservative 25; Mismatches 73; Indels 8; Gaps 2;

Oy 133 HPSPPEKE--LRKVAHLTGKSNSRSMPLEWETYSITVLISGVKKRGGLVINETGLYP 190
 ||| | :||| : : : | | | | |
Db 46 HPLQKHILTHCLIPAHALVGYPSKONSLLMRASDTDAFLRHGFSLSNNSILLIPTSGLYE 105
 ||| | :||| : : : | | | | |

191 YTSVFYFGGSCN-----NLPLSHKYVMNRSKVPDOLVMMECKMSYCITGGWMARSSY 244
 ||| | :||| : : : | | | | |
106 YTSOVVFSGECSRAPIPTPYTLAEHVOLESQQPPHYPLLAKSVYPGIGCFWVSMT 165

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QY      245 GAVENLTASADHLVYNVSELSLVNFEESQTFEGLYKL 281
      ||||| : | : | : | : | : | : | : | : | : | : |
Db      166 QGAVFLLSKDQLSTHTDGTSHLHFSPSSVFFGAFAL 202

RESULT 6
JH0309
tumor necrosis factor beta precursor - rabbit
N:Alternate names: Lymphotoxin; TNF beta
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0309; PNM0098
R:Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A:Title: Structural analysis of the rabbit TNF locus, containing the genes encoding T
A:Reference number: JH0309; MUID:9106534; PMID:2249779
A:Accession: JH0309
A:Molecule type: DNA
A:Residues: 1-197 <SR>
A:Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31483.1; PID:g165755;
R:Shakhov, A.N.; Kuprash, D.V.; Turetskaya, R.L.; Azizov, M.M.; Andreyeva, A.V.; Nedo
Mol. Biol. (Mosk.) 23, 1743-1750, 1989
A:Title: Cloning and structural analysis of the genes, coding for rabbit tumor necros
A:Reference number: PNM0098; MUID:90220566; PMID:2633043
A:Accession: PNM0098
A:Molecule type: mRNA
A:Residues: 1-197 <SR>
A:Cross-references: GB:X5745; NID:g297167; PIDN:CAA39275.1; PID:g297168
C:Genetics:
A:introns: 25/3; 61/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F.1-26/Domain: signal sequence #status predicted <SIG>
F.27-197/Product: Lymphotoxin #status predicted <MTR>

Query Match      13.1%; Score 200; DB 1; Length 197;
Best Local Similarity 26.0%; Pred. No. 9.6e-08;
Matches 61; Conservative 28; Mismatches 82; Indels 64; Gaps 7;

QY      55 PPPPPPPPLPPLPLPKKRGNSHTGCLVMFMVLVALVGLGMPQLFLKELAEI 114
      ||||| : | : | : | : | : | : | : | : | : | : |
Db      19 PPPPGAGGLPFAEPFPPSAAR----- 38

QY      115 RESTSQMHTASLEKQIGHPSPEPKEKLRKVAHLTKSNSRSMPLFME-DTYGIYVLSG 173
      ||||| : | : | : | : | : | : | : | : | : | : |
Db      39 -----NAQRRLQKHGHST-----LKRPAHLVGDPSKQD-SLRWRANTDRAFLRHG 83

QY      174 VKRYKGLVINETGLFYVTSKVFYRGQSCN-----NLPLSHKVMNSKYPQDLYVMEG 227
      ||||| : | : | : | : | : | : | : | : | : | : |
Db      84 FSLSNSLILVPSGSLFYFSQVVSFGSGCSKAVPTPLYLALAEHQVLSQSYFHVPLLSA 143

QY      228 KMASTCTTGG-MMARSSYLCAVFNLTADHLVYNVSELSLVNFEESQTFEGLYKL 281
      ||||| : | : | : | : | : | : | : | : | : | : |
Db      144 Q-KSVCPDQPGPMWRSYVGAVFLLTQGDQLSTHTDIAHLLSPSSVFFGAFAL 197

RESULT 7
OMHUX
Lymphotoxin alpha precursor - human
N:Alternate names: Lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 07-Jul-1995 #text_change 16-Jun-2000
C:Accession: A02755; S36154; I54482; A93350; B38877; A91906; A61478; S26951; A01645;
R:Nedwin, G.E.; Jarrett-Nedwin, J.; Smith, D.H.; Maylor, S.L.; Sakaguchi, A.Y.; Goedd
J. Cell. Biochem. 29, 171-181, 1985
A:Title: Structure and chromosomal localization of the human lymphotoxin gene.
A:Reference number: A92755; MUID:86086150; PMID:3001109
A:Accession: A92755
A:Molecule type: DNA
A:Residues: 1-59; 'N', 61-205 <NED>
R:Ritts, F.U.M.; Bouguenel et, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Ju
Nature Genet. 3, 137-145, 1993

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A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within
 A:Reference number: S36152; MUID:93272029; PMID:8499947
 A:Accession: S36154
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-12, 'R', 14-205 <IRI>
 A:Cross-references: EMBL:215026; NID:937211; PIDN:CAA78746.1; PID:937213
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 R:Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.
 Immunogenetics 33, 50-53, 1991
 A:Title: Haplotypic polymorphisms of the TNF gene
 A:Reference number: 154482; MUID:91139175; PMID:1671667
 A:Accession: 154482
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-124, 'P', 126-205 <RES>
 A:Cross-references: GB:M55913; NID:9339742; PIDN:AA559455.1; PID:9339743
 A:Experimental source: ancestral haplotype 57.1
 A:Note: 59-Aan was also found (ancestral haplotype 8.1)
 R:Gray, P.W.; Agarwal, B.B.; Benton, C.V.; Bringham, T.S.; Henzel, W.J.; Jarrett, J.A.;
 Nature 312, 721-724, 1984
 A:Title: Cloning and expression of cDNA for human lymphotoxin, a lymphokine with tumour
 A:Reference number: A93350; MUID:85086243; PMID:6334807
 A:Accession: A93350
 A:Molecule type: mRNA
 A:Residues: 1-205 <GRA>
 A:Cross-references: GB:X01393; NID:934444; PIDN:CAA25649.1; PID:934445
 A:Experimental source: lymphoblastoid cell line RPMI-1788
 R:Goeddel, D.V.; Agarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Palladino, M.A.;
 Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986
 A:Title: Tumor necrosis factors: gene structure and biological activities.
 A:Reference number: A32877; MUID:87217059; PMID:3472740
 A:Accession: B32877
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 35-205 <GOE>
 R:Kobayashi, Y.; Miyamoto, D.; Asada, M.; Ohtsuka, M.; Osawa, T.
 J. Biochem. 100, 727-733, 1986
 A:Title: Cloning and expression of human lymphotoxin mRNA derived from a human T cell hy
 A:Reference number: A91906; MUID:87057135; PMID:3536896
 A:Accession: A91906
 A:Molecule type: mRNA
 A:Residues: 1-59, 'N', 61-205 <KOB>
 A:Cross-references: GB:D00102; NID:9219913; PIDN:BA00064.1; PID:9219914
 A:Note: the authors translated the codon TAT for residue 156 as Thr and ACC for residue
 R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
 Lymphokine Res. 7, 175-185, 1988
 A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
 A:Reference number: A61478; MUID:88301617; PMID:2841543
 A:Accession: A61478
 A:Molecule type: protein
 A:Residues: 56-79, 86-95, 'X', 97, 'X', 99, 119-151, 'XX', 154-162, 'X', 164, 'X', 166, 'X', 168, 'X', 1
 01gt, C.G.; Maurer-Poggy, I.; Adolf, G.R.
 J. Biol. Chem. 267, 314, 85-88, 1992
 A:Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylation
 A:Reference number: S26951; MUID:93083656; PMID:1451807
 A:Accession: S26951
 A:Molecule type: protein
 A:Residues: 35-59, 'N', 61-205 <VOI>
 A:Note: 60-Thr was also found
 R:Fukushima, K.; Matanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K.
 Arch. Biochem. Biophys. 304, 144-153, 1993
 A:Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by CHO
 A:Reference number: S34742; MUID:93311995; PMID:8323280
 A:Accession: S34742
 A:Contents: annotation
 C:Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction,
 while having no detrimental effect on normal cells. It can also act synergistically with
 C:Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of differ
 ent activities but are produced by different cell types and have different induction ki
 C:Genetics:
 A:Gene: GDB:UTA; LT; TNFB
 A:Cross-references: GDB:120442; OMIM:153440
 A:Map position: 6p21.3-6p21.3

A:introns: 33/3; 69/1
 A:Note: the first intron occurs before the initiator codon
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophage
 F1-34/Domain: signal sequence #status predicted <SIG>
 F1-35-205/Product: lymphotoxin #status predicted <MAT>
 F1-36/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F1-36/Binding site: carbohydrate (Asn) (covalent) #status experimental
 Query Match 12.5%; Score 191; DB 1; Length 205;
 Best Local Similarity 27.4%; Pred. No. 1, le-06;
 Matches 57; Conservative 33; Mismatches 90; Indels 26; Gaps 4;
 81 LCLVWFVYVALYGL-GLGFEOLFLKELAELENESTQMHTRSSLEKQIGHPSPPE 139
 19 LLLGLGLLVLPAGQGLPGVG-----LTPSAQFARQPKMHLAHS----- 59
 140 KRELKRVNHLTGKSNRSRNPLEDYTGIVLLSGYKKGGLVNETGYFYYSKYFRG 199
 60 --TLKPAHLIDPDKNSLNRANTDRAFLDGFSLNSLSLVPSTGYFYYSKYFRG 117
 200 Q-----SCNNPLSHKRYMRSKYPODLVMEGKMSTCTGOMARSSYLGAFFNLS 253
 118 KAYSPEATSSPLYLHNEVGLFSSQYFHHPLLSQKMYVPGQEPMLHMGAAFLQ 177
 254 ADHLYVNSLSLVNFEESQTFGLYKL 281
 178 GOLSTHTGTGIRHLYLSPSTVEFGAFAL 205
 RESULT 8
 JQ1344
 tumor necrosis factor alpha precursor - horse
 N:Alternate names: cachectin; TNF alpha
 C:Species: Equus caballus (domestic horse)
 C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #extl-change 04-Feb-2000
 C:Accession: JQ1344
 R:Su, X.; Morris, D.D.; McGraw, R.A.
 Gene 107, 319-321, 1991
 A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosi
 A:Reference number: JQ1344; MUID:92084125; PMID:1748301
 A:Accession: JQ1344
 A:Molecule type: DNA
 A:Residues: 1-234 <SUX>
 A:Cross-references: GB:M64087; NID:9164244; PIDN:AAA30959.1; PID:9164245
 C:Comment: This protein is an important proximal mediator of endotoxemia.
 C:Genetics:
 A:Gene: TNF-alpha
 A:introns: 62/3; 79/1; 95/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
 F1-78-334/Product: tumor necrosis factor alpha #status predicted <TUM>
 F1-19-20/Binding site: myristate (Lys) (covalent) #status predicted
 F1-92/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F1-46-178/Disulfide bonds: #status predicted
 Query Match 12.2%; Score 186.5; DB 1; Length 234;
 Best Local Similarity 27.2%; Pred. No. 1, le-06;
 Matches 62; Conservative 36; Mismatches 99; Indels 31; Gaps 10;
 72 KKRGNSTGICLVWFVYVALYGLGMPDFHL-----OKELAEIRSTQMHRA 124
 20 KAGGPGGSRCLCLISFSL--LVAGATTFLFLHFGVGPQREGLPAPAFSINPL--A 75
 125 SSLERQIGHSPSPPEKELRKVAHLTGKSNRSRNPLEDYTGIVLLSGYKKGGLV 183
 76 QTLRSSRRPSPDK-----VAHYVANNQAGQ--LQWLSGRANMLANGVLTQNLQV 127
 184 NETGLYFVYSKYVFRGSC--NNPLSHKRYMRSKYPODLVMEGKMSTCTT----- 235
 128 PLDGLYLYISQVLEFGQGPSTHVLTHIRSLAIVSPSKVNLGA--IKSPCHTESPEQA 186
 236 -GOMARSSYLGAFFNLSADHLYVNSLSLVNFEES-QTFGLYKL 281

Db 187 EAKPWYEPYLGAVFQLEKGDQLSAEINQPYLDPFAESGQYVFGLIAL 234

RESULT 9

S12606

tumor necrosis factor alpha precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C:Accession: S12606; S17290; S18965; 146659

R:Drum, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.

Nucleic Acids Res. 18, 5564, 1990

A:Title: Gene sequence of porcine tumor necrosis factor alpha.

A:Reference number: S12606; MUID:91016861; PMID:2216741

A:Accession: S12606

A:Molecule type: DNA

A:Residues: 1-232 <DRE>

A:Cross-references: EMBL:X54001; NID:92135; PIDN:CAA38639.1; PID:92136

R:Kuhnert, P.; Muehlrich, C.; Peterhans, E.; Pauli, U.

Gene 102, 171-178, 1991

A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal

A:Reference number: S17289; MUID:91340150; PMID:1874444

A:Accession: S17290

A:Molecule type: DNA

A:Residues: 1-232 <KDH>

A:Cross-references: EMBL:X54859; NID:92132; PIDN:CAA38639.1; PID:92134

R:Choi, C.S.; Mollitor, T.W.; Lin, G.F.; Murrain, M.P.

submitted to the EMBL Data Library, January 1991

A:Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis fa

A:Reference number: S18965

A:Accession: S18965

A:Molecule type: mRNA

A:Residues: 1-232 <CHO>

A:Cross-references: EMBL:X57321; NID:92137; PIDN:CAA40591.1; PID:92138

R:Pauli, U.; Beutler, B.; Peterhans, E.

Gene 81, 185-191, 1989

A:Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction

A:Reference number: 146659; MUID:90034181; PMID:2478420

A:Accession: 146659

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 44-232 <PAU>

A:Cross-references: GB:M29079; NID:9164694; PIDN:AAA31128.1; PID:9164695

A:Genetics:

A:Introns: 62/3; 78/1; 93/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myri

F:1-77/Domain: propeptide #status predicted <PRO>

F:78-232/Product: tumor necrosis factor alpha #status predicted <MAT>

F:19-20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carbonylate (Ser) (covalent) #status predicted

F:144-176/Disulfide bonds: #status predicted

Query Match 12.2%; Score 185.5; DB 1; Length 232;

Best Local Similarity 28.7%; Pred. No. 1.3e-06;

Matches 68; Conservative 26; Mismatches 92; Indels 51; Gaps 10;

Db 72 KKGHNSHTGICLVFNFVVALVGLGFMFHL-----QKE-----LAELR 115

Db 20 KAGPQSGSRICLSTLSFSL--LVAGATTFLCLHFEVIGPKKEFPAPLSINPLAQGL 77

Db 116 ESTGOMHTASLEQIGHPSPPEKKELRKVAHLTGKSNKSMPLWEDTGYVLL--SGV 174

Db 78 RSSQSOTSD-----KPAHAAVANYAKAGC--LQWOSGYANMLANGV 116

Db 175 KYKGGVIVNETGLFYFYSKYFRGQSC--NNLPLSHKVMYRNKSKYPQDLVMEGKMMSY 232

Db 117 KLNQNLVPTDGLYLYISQLFRGQSGPSTNVPLFTHIRISIAVSY--QTKNKLMSAISPS 175

Db 233 C-----TTGOMARRSSYLGAVFNLTSADHLYVNVSELSLVNFEES--QTFEGLYKL 281

Db 176 CORETPGAEAKPWYEPYLGAVFQLEKDRLSAEINPDYLDPAESGQYVFGLIAL 232

RESULT 10

S17289

tumor necrosis factor beta precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S17289

R:Kuhnert, P.; Muehlrich, C.; Peterhans, E.; Pauli, U.

Gene 102, 171-178, 1991

A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative a

A:Reference number: S17289; MUID:91340150; PMID:1874444

A:Accession: S17289

A:Molecule type: DNA

A:Residues: 1-204 <KUH>

A:Cross-references: EMBL:X54859; NID:92132; PIDN:CAA38638.1; PID:92133

C:Genetics:

A:Introns: 32/3; 68/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage

F:1-33/Domain: signal sequence #status predicted <SIG>

F:34-204/Product: tumor necrosis factor beta #status predicted <MAT>

Query Match

Best Local Similarity 32.7%; Score 184; DB 1; Length 204;

Matches 53; Conservative 22; Mismatches 75; Indels 12; Gaps 6;

Db 130 QIGHPSPPE--KELRKVAHLTGKSNKSMPLWEDTGYVLLSGYKKGGLVYNET 186

Db 45 QPAHQHPKHLARGLTKPAHLVGPSTPD--SLKWRANTDRAFLRHGFLSNLSILVPTS 103

Db 187 GLTFYKSVYFRGQSC-----NNLPLSHKVMYRNKSKYPQDLVMEGKMMSYCTTGO--NW 239

Db 104 GLTFYKSVYFRGQSC-----NNLPLSHKVMYRNKSKYPQDLVMEGKMMSYCTTGO--NW 239

Db 240 ARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 163 VRSYQGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLYKL 281

Db 129 YIAHEVQLEFSPYPPHVPILLSAQ-KSCVCPGPGPMVRSVYQGAVFLLTRGDLSHTHTDGI 187
 QY 265 SLVNFEESSQTFPGLYKL 281
 Db 188 SHLLSPSSVFFGAFAL 204

RESULT 12

S24642
 tumor necrosis factor alpha precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C:Accession: I46047; S24642

R:Clutls, I.; Cleuter, Y.; Kettmann, R.; Burry, A.; Droogmans, L.

CyCline 5, 336-341, 1993

A>Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tu

A:Reference number: I46046; MWID:94083525; PMID:8260599

A:Accession: I46047

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-233 <CL2>

A:Cross-references: EMBL:Z14137; NID:9796; PIDN:CAA78511.1; PID:9798

C:Genetics:

Gene: TNFA

Introns: 62/3; 78/1; 94/1

Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

E:20/Binding site: myristate (lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

Query Match 12.0%; Score 183; DB 1; Length 233;
 Best Local Similarity 29.4%; Pred. No. 2e-06;
 Matches 65; Conservative 27; Mismatches 111; Indels 18; Gaps 8;

QY 72 KRGNSHSTGLCLVMEFVLAIVGLMFOFLHQKELAEKRETSQMHRTASLEKQI 131
 Db 20 KAGGPGGSRCLCLSLFSL--LVAGATTLFCLHGVGPQEEPSGPGSPINLVYOTI 77
 QY 132 GHSPPEPEKELKVAHLTGKNSRSMPEMEDTYGIVLL-SGVKKYKGGVLYNETGLXF 190
 Db 78 RSSQSQSNK---PVAHVVAADINSPOG-LRMWDSYANMALMANGVKLEDQNLVVPADGLYL 133
 QY 191 VYSKYFRQSCNLP--LSHKYMANSTYPODLVMEGKMSYC-----TTGQMMAR 241
 Db 134 IYSQVLFRCQGPSPFLFHTISRIYAVS-QTKVNLISAIKSPCHRETPENAEAPWYE 192
 QY 242 SSYLGAFFNLTSAADHLVYVNSELSLVNFEES-OTFFGLYKL 281
 Db 193 PIYGGVFOLEKGRSLAEINLPDYIDYAESGOVYFGITALL 233

ULT 13

UN

tumor necrosis factor alpha precursor [validated] - human

N:Alternate names: cachectin; TNFA

C:Species: Homo sapiens (man)

C>Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000

C:Accession: A93585; S36153; A93551; A44189; B61478; I53111; S62610; I54522; A01646; B23

R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.

Nucleic Acids Res. 13, 6361-6373, 1985

A>Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chro

A:Reference number: A93585; MWID:86016093; PMID:2995927

A:Accession: A93585

A:Molecule type: DNA

A:Residues: 1-233 <NED>

A:Cross-references: GB:X02910; GB:X02159; NID:937209; PIDN:CAA26669.1; PID:937210

R:Tris, F.J.M.; Bouguetel, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka

Nature Genet. 3, 137-145, 1993

A>Title: Dense Ali clustering and a potential new member of the NFkappaB family within a

A:Reference number: S36152; MWID:93272029; PMID:8499947

A:Accession: S36153

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-233 <IRI>

A:Cross-references: EMBL:Z15026; NID:937211; PIDN:CAA78745.1; PID:937212

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992

R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M

Nature 312, 724-729, 1984

A>Title: Human tumour necrosis factor: precursor structure, expression and homology t

A:Reference number: A93551; MWID:85086244; PMID:6392892

A:Accession: A93551

A:Molecule type: mRNA

A:Residues: 1-233 <PEN>

A:Cross-references: GB:X02910; GB:X02159; NID:937209; PIDN:CAA26669.1; PID:937210

A>Note: this protein was isolated from the monocytic-like cell line HL-60 from a promy

R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdale, J.N

Science 228, 149-154, 1985

A>Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.

A:Reference number: A44189; MWID:85142190; PMID:3856324

A:Accession: A44189

A:Molecule type: mRNA

A:Residues: 1-62, 'S', 64-233 <NAN>

A:Cross-references: GB:M10988; NID:9339737; PIDN:AAA61198.1; PID:9339738

R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.;

Lymphokine Res. 7, 175-185, 1988

A>Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta

A:Reference number: A61478; MWID:88301617; PMID:2841543

A:Accession: B61478

A:Molecule type: protein

A:Residues: 83-102,109-119,121-128,'X',130-131,142-144,'X',146,'xxx',150-152,159-174;

R:Harmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashim

Eur. J. Biochem. 152, 515-522, 1985

A>Title: Molecular cloning and expression of human tumor necrosis factor and compats

A:Reference number: I53111; MWID:86030296; PMID:3932069

A:Accession: I53111

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-233 <NAN>

A:Cross-references: GB:M26331; NID:9339763; PIDN:AAA36758.1; PID:9339764

A:Experimental source: U-937 cells

R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.

Eur. J. Biochem. 235, 431-437, 1996

A>Title: O-Glycosylated species of natural human tumor necrosis factor-alpha.

A:Reference number: S62610; MWID:96202967; PMID:8631363

A:Accession: S62610

A:Molecule type: protein

A:Residues: 77-99 <TAK>

R:D'Alfonso, S.; Richiardi, P.M.

Immunogenetics 39, 150-154, 1994

A>Title: A polymorphic variation in a putative regulation box of the TNFA promoter re

A:Reference number: I54522; MWID:94102809; PMID:7903959

A:Accession: I54522

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-8 <DAL>

A:Cross-references: GB:S68530; NID:9544751

R:Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.

J. Exp. Med. 176, 1053-1062, 1992

A>Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific

A:Reference number: A59163; MWID:93018820; PMID:1402651

C:Contents: annotation; identification of myristylated lysines

R:Aggarwal, B.B.; Kohr, W.J.; Haas, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Br

J. Biol. Chem. 260, 2345-2354, 1985

A>Title: Human tumor necrosis factor: Production, purification, and characterization.

A:Reference number: A92511; MWID:8510974; PMID:3871770

C:Contents: annotation; disulfide bond

C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induc

ut are produced by different cell types and have different induction kinetics.

C:Genetics:

A:Gene: GDB:TNF; TNFA

A:Cross-references: GDB:120441; OMIM:191160

A:Map position: 6p21.3-6p21.3

A:Introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macrophage activating factor; monomer; proinflammatory mediator
F:1-76/Domin: propeptide #status predicted <PRO>
F:77-233/Product: tumor necrosis factor #status experimental <MAT>
F:19,20/Binding site: myristate (Lys) (covalent) #status experimental
F:81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F:145-177/Disulfide bonds: #status experimental

Query Match 11.9%; Score 181; DB 1; Length 233;
Best Local Similarity 27.4%; Pred. No. 2,9e+06;
Matches 61; Conservative 32; Mismatches 112; Indels 18; Gaps 8;

OY 70 PLKRGHNSGCLLVNFMYVALVGLIGMPOLFHLQKEFLAELRESTSOMHTASSLEK 129
 | : | : | : | : | : | : | : | : | : | : | : | :
 18 PKRKGPGSGSRNCFLLSLFSFLI--VAGATTLFCILHHGVIGPGRREFPRDLSTLSPLAQ 75

OY 130 QIGHPPPEPEKKELRKVAHAHLGKSNSMSPLEMEDTGYIVLL-SGVYYKKGGVLINFTGL 188
Db 76 AVRSSTRPSPK---PYAHVVANPDASEQ-LQMNRRAHALLAGVELRDNQNLVPSEGL 131

OY 189 YFYVSRYVFYGQS--NNLP.LSHKYRNKRNPODYLMMEGKMASYC-----TTGQMW 239
Db 132 YLIYSQYLFRKGQGSPRHVLLTFRTISRAYSV-QTKNLSAISKPQGRETPEGAEAKPW 190

OY 240 ARSSYLGAVNFLTSADHLLYNVSELISLVNEES-QTFPGLYKL 281
Db 191 YEPIYLGVEPFOLKGDRLSAEINRPDYLDFAESQGVFFITAL 233

RESULT 14

A:34043
A:Accession: A34043
Description: hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment)
C:Species: Owenia fusiformis
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000
C:Accession: A34043 #sequence_revision 07-Jun-1990
R:Bakalaria, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
Biochem. Biophys. Res. Commun. 166, 66-73, 1990
A:Title: Presence in invertebrate genomes of sequences characterized by the repetition c
A:Reference number: A90159; MUID:90147742; PMID:2105723
A:Accession: A34043
A:Molecule type: DNA
A:Residues: 1-141 <BAK>
A:Cross-references: GB:M32217
A:Accession: B34043
A:Molecule type: DNA
A:Residues: 59-136 <BA2>
A:Cross-references: GB:M32217

Query Match 11.6%; Score 177; DB 2; Length 141;
Best Local Similarity 49.3%; Pred. No. 3.2e+06;
Matches 35; Conservative 6; Mismatches 28; Indels 2; Gaps 1;

OY 18 SASPMWAPGVLCPTSVRRRPGQRPPPPPPLPLPPPPPPLPLPLPLPKRRGNH 77
 | : | : | : | : | : | : | : | : | : | : | : | :
Db 6 SLTRPPRARIRIH 65

OY 78 STGIQLVMFE 88
 | : | : | : | : | : | : | : | : | : | : | : | :
Db 66 N-IDPLFRFF 74

RESULT 15

S22052
tumor necrosis factor alpha precursor - baboon
C:Species: Papio sp. (baboon)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: S22052
R:Sanjanwala, M.; Edwards, A.
submitted to the EMBL Data Library, September 1991
A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A:Reference number: S22052
A:Accession: S22052

[illegible]

Search completed: June 24, 2003, 11:08:51
Job time : 22.3505 secs

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